

16 1292 37.5 2192 2 Q491L5_AEDAE Q491L5 aedes aegypti
 17 1284 37.3 2249 1 DCR1L_DROME Q390U9 drosophila
 18 1283 37.2 2280 2 Q29AU1_DROPS Q29AU1 drosophila
 19 1151 33.4 1845 1 DCR1L_CAEEL P34529 caenorhabditis
 20 1106.5 32.1 1863 2 Q60M66_CAEER Q60M66 caenorhabditis
 21 902 26.2 2043 2 Q27IU2_DROME Q27IU2 drosophila
 22 896 26.0 2043 2 Q27IT7_DROSI Q27IT7 drosophila
 23 894 25.9 2043 2 Q27IT4_DROSI Q27IT4 drosophila
 24 894 25.9 2043 2 Q27IT9_DROSI Q27IT9 drosophila
 25 894 25.9 2043 2 Q27IT6_DROSI Q27IT6 drosophila
 26 894 25.9 2043 2 Q27IT8_DROSI Q27IT8 drosophila
 27 894 25.9 2043 2 Q27IU7_DROME Q27IU7 drosophila
 28 894 25.9 2043 2 Q27IU0_DROME Q27IU0 drosophila
 29 894 25.9 2043 2 Q27IU5_DROME Q27IU5 drosophila
 30 894 25.9 2043 2 Q27IU9_DROME Q27IU9 drosophila
 31 894 25.9 2043 2 Q27IU4_DROME Q27IU4 drosophila
 32 894 25.9 2043 2 Q27IU8_DROME Q27IU8 drosophila
 33 893 25.9 2043 2 Q27IU3_DROME Q27IU3 drosophila
 34 893 25.9 2043 2 Q27IT5_DROSI Q27IT5 drosophila
 35 892 25.9 2043 2 Q27IU6_DROME Q27IU6 drosophila
 36 886 25.8 2043 2 Q27IU1_DROSI Q27IU1 drosophila
 37 713 20.7 149 2 Q862N0_BOVIN Q862N0 bos taurus
 38 631 18.3 1658 2 Q174T8_AEDAE Q174T8 aedes aegypti
 39 624 18.1 1715 2 Q29IA3_DROPS Q29IA3 drosophila
 40 623 18.1 1658 2 Q491L4_AEDAE Q491L4 aedes aegypti
 41 616.5 17.9 1719 2 Q2Q3U0_DROYA Q2Q3U0 drosophila
 42 616.5 17.9 1719 2 Q2Q3U4_DROYA Q2Q3U4 drosophila
 43 612 17.8 1719 2 Q2Q3U1_DROYA Q2Q3U1 drosophila
 44 612 17.8 1719 2 Q2Q3U5_DROYA Q2Q3U5 drosophila
 45 612 17.8 1719 2 Q2Q3U3_DROYA Q2Q3U3 drosophila

ALIGNMENTS

RESULT 1

DICER_HUMAN

ID DICER_HUMAN Reviewed: 1912 AA.
 AC Q3UPY3; Q95943; Q9Q0Q2;
 DT 25-OCT-2002, integrated into UniProtKB/Swiss-Prot.
 DT 25-OCT-2002, sequence version 2.
 DT 24-JUL-2007, entry version 61.
 DE Endoribonuclease Dicer (EC 3.1.26.-) (Helicase with RNase motif)
 DE (Helicase-MOI).
 GN Name=DICER1; Synonyms=DICER, HERNA, KIAA0928;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (MRNA).
 RX MEDLINE=20246304; PubMed=10786632; DOI=10.1016/S0167-4781(99)00221-3;
 RA Matsuda S., Ichikotani T., Okuda T., Irimura T., Nakatsugawa S.,
 RA Hamaguchi M.;
 RT "Molecular cloning and characterization of a novel human gene (HERNA)
 RT which encodes a putative RNA-helicase.";

RL Blochin. Biophys. Acta 1490:163-169 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (MRNA).
 RC TISSUE=Lung;
 RA Provost P., Dishart D., Doucet D., Hermansson A., Frenedewey D.,
 RA Samuelsson B., Radmark O.;
 RT "RNA binding and processing by recombinant human Dicer.*";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
 RC TISSUE=Brain;
 RX MEDLINE=99246063; PubMed=10231032; DOI=10.1093/dnares/6.1.63;
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.*";
 RL DNA Res. 6:63-70 (1999).
 RN [4]
 RP SEQUENCE REVISION.
 RX MEDLINE=22158633; PubMed=12168954; DOI=10.1093/dnares/9.3.39;
 RA Miyajima N., Oikawa K., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual
 RT curation of 330 KIAA cDNA clones.";
 RL DNA Res. 9:99-106 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (MRNA) CP 1239-1912.
 RC TISSUE=Lung;
 RX MEDLINE=99162526; PubMed=10051636; DOI=10.1073/pnas.96.5.1881;
 RA Provost P., Samuelsson B., Radmark O.;
 RT "Interaction of 5-lipoxygenase with cellular proteins.*";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1881-1885 (1999).
 RN [6]
 RP INTERACTION WITH PIWILL.
 RX PubMed=14745716; DOI=10.1038/sj.embo.7400070;
 RA Tahbaz N., Kolb F.A., Zhang H., Jaroszyk K., Filipowicz W.,
 RA Holman T.C.;
 RT "Characterization of the interactions between mammalian PANI
 RT domain proteins and Dicer.*";
 RL EMBO Rep. 5:189-194 (2004).
 RN [7]
 RP PHOSPHORYLATION (LARGE SCALE ANALYSIS) AT TYR-654, AND MASS
 RP SPECTROMETRY.
 RX PubMed=15592455; DOI=10.1038/nbt1046;
 RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
 RA Zha X.-M., Polakiewicz R.D., Comb M.J.;
 RT "Immunofluorescence profiling of tyrosine phosphorylation in cancer
 RT cells.*";
 RL Nat. Biotechnol. 23:94-101 (2005).
 CC -I- FUNCTION: Involved in cleaving double-stranded RNA in the RNA
 CC interference (RNAi) pathway. It produces 21 to 23 bp dsRNAs
 CC (siRNAs) which target the selective destruction of homologous
 CC RNAs.
 CC -I- SUBUNIT: Interacts with PIWILL.
 CC -I- INTERACTION:
 CC Q5UL18:EIF2C1; NbExp=2; IntAct=EBI-395006, EBI-527363;
 CC Q9UKV8:EIF2C2; NbExp=1; IntAct=EBI-395006, EBI-528269;

CC Q8CJG0:EIF2c2 (xeno); NbExp=2; IntAct=EBI-395506, EBI-528299;
CC Q8TQY3:PMWILL; NbExp=1; IntAct=EBI-395506, EBI-527417;
CC Q15633:TARBP2; NbExp=4; IntAct=EBI-395506, EBI-978581;
CC -I- SIMILARITY: Belongs to the helicase family.
CC -I- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
CC -I- SIMILARITY: Contains 1 helicase ATP-binding domain.
CC -I- SIMILARITY: Contains 1 helicase C-terminal domain.
CC -I- SIMILARITY: Contains 1 PAZ domain.
CC -I- SIMILARITY: Contains 2 RNase III domains.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR ENBL; AB028449; BAA78691.1; ALT_INIT; mRNA.
DR ENBL; AJ132261; CB38057.2; -; mRNA.
DR ENBL; AB023145; BAA76772.2; ALT_INIT; mRNA.
DR UniGene; Hs.87889; -.
DR HSP; 067082; LOF2.
DR IntAct; Q9UPY3; -.
DR Ensembl; ENSG00000100697; Homo sapiens.
DR KEGG; hsa:23405; -.
DR HNCI; HNCI:17098; DICER1.
DR HPA; HPA000694; -.
DR MIM; 606241; gene.
DR PharmGKB; PA38437; -.
DR ArrayExpress; Q9UPY3; -.
DR GeneOnline; ENSG00000100697; Homo sapiens.
DR GO; GO:0005622; C:intracellular; NAS:UniProtKB.
DR GO; GO:0003729; F:double-stranded RNA binding; IDA:UniProtKB.
DR GO; GO:0005515; F:protein binding; IPI:IntAct.
DR GO; GO:0004529; F:ribonuclease III activity; IDA:UniProtKB.
DR GO; GO:0030423; F:RNA interference, targeting of mRNA for des. . .;
IEP:UniProtKB.
DR InterPro; IPR014001; DEAD-like_M.
DR InterPro; IPR011545; DEAD/DEAH_M.
DR InterPro; IPR001159; De_RNA_bd.
DR InterPro; IPR005034; DUF293.
DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR000999; RNase_III.
DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF03368; DUF293; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF02170; PAZ; 1.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR SMART; SM00487; HDHC; 1.
DR SMART; SM00359; DSRG; 1.
DR SMART; SM00490; HELIC; 1.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS50137; D3_RBD; 1.
DR PROSITE; PS51192; HELICASE_ATP_BIND_1; 1.
DR PROSITE; PS51194; HELICASE_CTER; 1.
DR PROSITE; PS50821; PAZ; 1.
DR PROSITE; PS50517; RNASE_3_1; 1.

DR PROSITE; PS50142; RNASE_3_2; 2.
PE 1: Evidence at protein level;
KW ATP-binding; Endonuclease; Helicase; Hydrolase; Nuclease;
KW Nucleotide-binding; Phosphorylation; Repeat; RNA-binding;
KW RNA-mediated gene silencing.
FT CHAIN 1 1912 Endoribonuclease Dicer.
FT /FTid=PRO_0000180470.
FT DOMAIN 41 217 Helicase ATP-binding.
FT DOMAIN 423 592 Helicase C-terminal.
FT DOMAIN 881 1032 PAZ.
FT DOMAIN 1266 1393 RNase III 1.
FT DOMAIN 1656 1814 RNase III 2.
FT DOMAIN 1839 1904 DRBM.
FT NR_BIND 34 41 ATP (Potential).
FT MOTIF 165 168 DECH box.
FT NOD_RES 654 654 Phosphoryrosine.
FT CONFLICT 65 80 VLLKELSTQIGGDFS -> STLLKSLTLQLGRTSA
FT (in Ref. 1).
FT CONFLICT 179 179 I -> F (in Ref. 1).
FT CONFLICT 185 185 N -> I (in Ref. 1).
FT CONFLICT 204 204 C -> W (in Ref. 1).
FT CONFLICT 208 208 E -> D (in Ref. 1).
FT CONFLICT 213 213 I -> F (in Ref. 1).
FT CONFLICT 383 384 QQ -> HS (in Ref. 1).
FT CONFLICT 482 483 KQ -> NT (in Ref. 1).
FT CONFLICT 539 539 D -> H (in Ref. 1).
SQ SEQUENCE 1912 aa; 217628 MW; 9963993d8b074f21 CRC64;

Query Match 100.0%; Score 3446; DB 1; Length 1912;
Best Local Similarity 100.0%; Pred. No. 4.8e-229;
Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLLGRMDSQSPSISYSSRTLGPNGLLIQALLTLNAGSDGNLERLEMLGSPFLKHAIT 60
Db 1259 QVLLGRMDSQSPSISYSSRTLGPNGLLIQALLTLNAGSDGNLERLEMLGSPFLKHAIT 1318

Qy 61 TLYLCTPDAAEGLSYRGRKVSQNLVRLGRKKGLSPRWVSIIDPPVNLMPGGTVVN 120
Db 1319 TLYLCTPDAAEGLSYRGRKVSQNLVRLGRKKGLSPRWVSIIDPPVNLMPGGTVVN 1378

Qy 121 QQNSITDREKQEMCKDMLANGKLDVEYDEDEEESLMRAPKEADVECDLFYQGE 180
Db 1379 QQNSITDREKQEMCKDMLANGKLDVEYDEDEEESLMRAPKEADVECDLFYQGE 1438

Qy 181 EIRFDINLMGSGAFVKKISLSPFTTDSAYENRPPKSSLSQMFSSDFEDFYSSMDA 240
Db 1439 EIRFDINLMGSGAFVKKISLSPFTTDSAYENRPPKSSLSQMFSSDFEDFYSSMDA 1498

Qy 241 MCYLPKSKAVEEDDFVGFWIPSEKNGVOTQSKISYDLTEQCIAKSIADCVALLG 300
Db 1499 MCYLPKSKAVEEDDFVGFWIPSEKNGVOTQSKISYDLTEQCIAKSIADCVALLG 1558

Qy 301 CYLETSGEAAQLFLCSLGKLVPIKTRKALPTRENNVQQQLSVSCAAASVAS 360
Db 1559 CYLETSGEAAQLFLCSLGKLVPIKTRKALPTRENNVQQQLSVSCAAASVAS 1618

Qy 361 SRSSVLDKSEYGCILKIPROMDFDPACKLIMLISFENPEKKINTRFKNAQLQAT 420

```

|||||
Db 1619 SRSSVLDSEYGLKIPPCMFDRPDADRTIMHLISGFENFEKINIRFKIKAYLLQAF 1678
QY 421 HASTHNTIIDCYQLRFLGDAILDYLLITKHLIEDPQHSGVLTDRSALVNNTIFASL 480
|||||
Db 1678 HASTHNTIIDCYQLRFLGDAILDYLLITKHLIEDPQHSGVLTDRSALVNNTIFASL 1738
QY 481 AVKIDYHRYFKAIVSPFLFHWIDFVQFLKKNKQNDSELRSSDEDEKEDIEVFKAM 540
|||||
Db 1738 AVKIDYHRYFKAIVSPFLFHWIDFVQFLKKNKQNDSELRSSDEDEKEDIEVFKAM 1798
QY 541 GDIFESLAGATYNDGNSLETWQVYTPMRPLIEKFSANVPSPHLELMEPEITAKFS 600
|||||
Db 1798 GDIFESLAGATYNDGNSLETWQVYTPMRPLIEKFSANVPSPHLELMEPEITAKFS 1858
QY 601 PAERTYDGRVNTVEVVGKGFVGSRSTRIAKSAAPRALSLKANKQVQVWS 654
|||||
Db 1858 PAERTYDGRVNTVEVVGKGFVGSRSTRIAKSAAPRALSLKANKQVQVWS 1912

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RESULT 2

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AMQHO_CRIGR
ID AMQHO_CRIGR Unreviewed; 1917 AA.
AC AMQHO;
DT 12-DEC-2006, integrated into UniProtKB/TrEMBL.
DT 12-DEC-2006, sequence version 1.
DT 24-JUL-2007, entry version 5.
DE DICER.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Cricetidae; Cricetinae; Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallerstorfer D.;
RL Submitted (SEP-2006) to the EMBL/GenBank/DDBJ databases.
CC -----
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CC -----
DR EMBL; EFC31271; ABK28790.1; -, mRNA.
DR GO; GO:0005622; C:intracellular; IEA:InterPro.
DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA:InterPro.
DR GO; GO:0004386; F:helicase activity; IEA:InterPro.
DR GO; GO:0004525; F:ribonuclease III activity; IEA:InterPro.
DR GO; GO:0004396; F:RNA processing; IEA:InterPro.
DR InterPro; IPR014001; DEAD-like_M.
DR InterPro; IPR011545; DEAD/DEAH_M.
DR InterPro; IPR001159; Dc_RNA_bd.
DR InterPro; IPR003034; DUF293.
DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR000999; RNase_III.
DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.

```